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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
10/669,781	09/24/2003	Juha Apajalahti	79428	6390
22242	7590	10/25/2006	EXAMINER	
FITCH EVEN TABIN AND FLANNERY 120 SOUTH LA SALLE STREET SUITE 1600 CHICAGO, IL 60603-3406				FRONDA, CHRISTIAN L
ART UNIT		PAPER NUMBER		
				1652

DATE MAILED: 10/25/2006

Please find below and/or attached an Office communication concerning this application or proceeding.

<b>Office Action Summary</b>	<b>Application No.</b>	<b>Applicant(s)</b>	
	10/669,781	APAJALAHTI ET AL.	
	Examiner Christian L. Fronda	Art Unit 1652	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --  
**Period for Reply**

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) OR THIRTY (30) DAYS, WHICHEVER IS LONGER, FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

#### Status

- 1) Responsive to communication(s) filed on 28 August 2006.
- 2a) This action is FINAL.                    2b) This action is non-final.
- 3) Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

#### Disposition of Claims

- 4) Claim(s) 1-12 is/are pending in the application.
- 4a) Of the above claim(s) \_\_\_\_\_ is/are withdrawn from consideration.
- 5) Claim(s) \_\_\_\_\_ is/are allowed.
- 6) Claim(s) 1-12 is/are rejected.
- 7) Claim(s) \_\_\_\_\_ is/are objected to.
- 8) Claim(s) \_\_\_\_\_ are subject to restriction and/or election requirement.

#### Application Papers

- 9) The specification is objected to by the Examiner.
- 10) The drawing(s) filed on 24 October 2003 is/are: a) accepted or b) objected to by the Examiner.  
 Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).  
 Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).
- 11) The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

#### Priority under 35 U.S.C. § 119

- 12) Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).
- a) All    b) Some \* c) None of:
  1. Certified copies of the priority documents have been received.
  2. Certified copies of the priority documents have been received in Application No. 10/251,503.
  3. Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

\* See the attached detailed Office action for a list of the certified copies not received.

#### Attachment(s)

- 1) Notice of References Cited (PTO-892)
- 2) Notice of Draftsperson's Patent Drawing Review (PTO-948)
- 3) Information Disclosure Statement(s) (PTO/SB/08)  
 Paper No(s)/Mail Date 08/23/06.
- 4) Interview Summary (PTO-413)  
 Paper No(s)/Mail Date. \_\_\_\_\_.
- 5) Notice of Informal Patent Application
- 6) Other: RSL Error Report.

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### **DETAILED ACTION**

1. Claims 1-12 are pending and under consideration in this Office Action.
2. The rejection of claim 10 under 35 U.S.C. 112, second paragraph, as being indefinite has been withdrawn in view of applicants' arguments and amendment to the claim filed 08/28/2006.

### ***NUCLEOTIDE AND/OR AMINO ACID SEQUENCE DISCLOSURES***

3. This application fails to comply with the requirements of 37 CFR §§ 1.821 through 1.825 for the reason(s) set forth: certain errors were detected by the STIC Biotechnology Systems Branch. Please see the attached paper **RAW SEQUENCE LISTING ERROR REPORT**.

### ***Claim Rejections - 35 U.S.C. § 112, 1st Paragraph***

4. The following is a quotation of the first paragraph of 35 U.S.C. 112:  
The specification shall contain a written description of the invention, and of the manner and process of making and using it, in such full, clear, concise, and exact terms as to enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the same and shall set forth the best mode contemplated by the inventor of carrying out his invention.
5. Claims 1-12 are rejected under 35 U.S.C. 112, first paragraph, because the specification, while being enabling for an isolated nucleic acid of SEQ ID NO: 1, an isolated host cell transformed with a nucleic acid of SEQ ID NO: 1, and a method for identifying a nucleic acid molecule which encodes a phytase using SEQ ID NO: 1, and a method for the production of the nucleic acid sequence of SEQ ID NO: 1 using the specific PCR primers listed on page 25 of the specification; does not reasonably provide enablement for any nucleic acid that hybridizes to SEQ ID NO: 1 under any high stringency conditions and any method for the production of any nucleic acid which encodes a phytase using any two or more PCR primers which hybridize to SEQ ID NO: 1 or to any complement of SEQ ID NO: 1. The specification does not enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and/or use the invention commensurate in scope with these claims.

Applicants' arguments filed 08/28/2006 have been fully considered but are not

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persuasive. The examiner respectfully disagrees with applicants' position that one of ordinary skill in the art would understand what conditions are needed to provide high stringency for Southern blotting.

The nature and breadth of the claims encompass any nucleic acid that hybridizes to SEQ ID NO: 1 under any high stringency conditions. Applicants have not sufficiently defined the conditions under which the hybridizations are to take place. Nucleic acid hybridization assays are extremely sensitive to the conditions in which they are performed. The buffer composition, pH, temperature, length of time, salt concentrations, quality and source of template nucleic acid, are all variables which determine the reproducibility of a given hybridization experiment.

Given the unpredictability of the art and the nature of hybridization experiments in general, it is not sufficient to merely cite hybridization without a clear and explicit recitation of the conditions associated with the hybridization. For example, the definition of stringency as it pertains to hybridization conditions is subject to interpretation and is different from laboratory to laboratory. Therefore, without a clear and explicit recitation of the conditions which were actually used by Applicants in isolating the claimed polynucleotides which hybridize to the disclosed sequences, the skilled artisan would not be able to practice the claimed invention and would not be reasonably apprised of the metes and bounds of the claimed invention. Without such guidance, the experimentation left to those skilled in the art is undue. Including in the claims the exact nature of the hybridization conditions, such as salt concentration and temperature, would aid in overcoming this portion of the rejection.

### *Conclusion*

6. No claim is allowed.

7. **THIS ACTION IS MADE FINAL.** Applicant is reminded of the extension of time policy as set forth in 37 CFR 1.136(a).

A shortened statutory period for reply to this final action is set to expire THREE MONTHS from the mailing date of this action. In the event a first reply is filed within TWO MONTHS of the mailing date of this final action and the advisory action is not mailed until after the end of the THREE-MONTH shortened statutory period, then the shortened statutory period will expire on the date the advisory action is mailed, and any extension fee pursuant to 37 CFR 1.136(a) will be calculated from the mailing date of the advisory action. In no event, however, will the statutory period for reply expire later than SIX MONTHS from the mailing date of this final action.

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8. Any inquiry concerning this communication or earlier communications from the examiner should be directed to Christian L Fronda whose telephone number is (571)272-0929. The examiner can normally be reached Monday-Friday between 9:00AM - 5:00PM. If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Ponnathapura N Achutamurthy can be reached on (571)272-0928. The fax phone number for the organization where this application or proceeding is assigned is (571)273-8300.

9. Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see <http://pair-direct.uspto.gov>. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free).

CLF

  
TEKCHAND SAIDHA  
PRIMARY EXAMINER

## **STIC Biotechnology Systems Branch**

### **RAW SEQUENCE LISTING ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/669,781A  
Source: IFW/6  
Date Processed by STIC: 8/30/06

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.4.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm>), EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):  
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06



IFW16

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/669,781A

DATE: 08/30/2006

TIME: 10:14:33

Input Set : F:\6031.79428 sequence.listing.ST25.txt  
Output Set: N:\CRF4\08302006\J669781A.raw

3 <110> APPLICANT: Finnfeeds International, Ltd.  
 5 <120> TITLE OF INVENTION: Phytase from *Bacillus subtilis*, gene encoding said phytase,  
 6 method for its production and use  
 8 <130> FILE REFERENCE: 79428  
 10 <140> CURRENT APPLICATION NUMBER: 10/669,781A see pp 1-10  
 11 <141> CURRENT FILING DATE: 2003-09-24  
 13 <160> NUMBER OF SEQ ID NOS: 36  
 15 <170> SOFTWARE: PatentIn version 3.3

## ERRORED SEQUENCES

E--> 17 <210> SEQ ID NO: ~~SEQ ID NO+1~~ do not insert alphabetical headings. The CRF Software will insert them for clarity.  
 18 <211> LENGTH: 1290  
 19 <212> TYPE: DNA  
 20 <213> ORGANISM: *Bacillus subtilis*; Strain: B13  
 23 <220> FEATURE:  
 24 <221> NAME/KEY: CDS  
 25 <222> LOCATION: (91)..(1239)  
 27 <400> SEQUENCE: 1  
 28 cacatttgac aattttcaca aaaacttaac actgacaatc atgttatataat gttacaattg 60  
 30 aagtgcacgt tcataaaagg aggaagtaaa atg aat cat tca aaa aca ctt ttg 114  
 31 Met Asn His Ser Lys Thr Leu Leu  
 32 1 5  
 34 tta acc gcg gcg gcc gga ctg atg ctc aca tgc ggt gcg gtg tct tcc 162  
 35 Leu Thr Ala Ala Gly Leu Met Leu Thr Cys Gly Ala Val Ser Ser  
 36 10 15 20  
 38 cag gca aag cat aag ctg tcc gat cct tat cat ttt acc gtg aat gca 210  
 39 Gln Ala Lys His Lys Leu Ser Asp Pro Tyr His Phe Thr Val Asn Ala  
 40 25 30 35 40  
 42 gcg gcg gaa acg gaa ccg gtt gat acg gcc ggt gac gcg gct gat gat 258  
 43 Ala Ala Glu Thr Glu Pro Val Asp Thr Ala Gly Asp Ala Ala Asp Asp  
 44 45 50 55  
 46 cct gcg att tgg ctg gac ccc aag act cct cag aac agc aaa ttg att 306  
 47 Pro Ala Ile Trp Leu Asp Pro Lys Thr Pro Gln Asn Ser Lys Leu Ile  
 48 60 65 70  
 50 acg acc aat aaa aaa tca ggt tta gtc gtt tac agc ctt gat ggt aag 354  
 51 Thr Thr Asn Lys Lys Ser Gly Leu Val Val Tyr Ser Leu Asp Gly Lys  
 52 75 80 85  
 54 atg ctt cat tcc tat aat acc ggg aag ctg aac aat gtc gat atc cgt 402  
 55 Met Leu His Ser Tyr Asn Thr Gly Lys Leu Asn Asn Val Asp Ile Arg  
 56 90 95 100  
 58 tat gat ttt ccg ttg aac ggc aaa aaa gtc gat atc gcg gca tcc 450

*Does Not Comply  
Corrected Diskette Needed*

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/669,781A

DATE: 08/30/2006

TIME: 10:14:33

Input Set : F:\6031.79428 sequence.listing.ST25.txt  
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60	105	110	115	120	
62	aat cgg tct gaa gga aaa aat acc att gag att tac gct att gat gga				498
63	Asn Arg Ser Glu Gly Lys Asn Thr Ile Glu Ile Tyr Ala Ile Asp Gly				
64	125	130	135		
66	aaa aac ggc aca tta caa agc atg aca gat cca gac cat ccg att gca				546
67	Lys Asn Gly Thr Leu Gln Ser Met Thr Asp Pro Asp His Pro Ile Ala				
68	140	145	150		
70	aca gca att aat gag gta tac ggt ttt acc tta tac cac agt caa aaa				594
71	Thr Ala Ile Asn Glu Val Tyr Gly Phe Thr Leu Tyr His Ser Gln Lys				
72	155	160	165		
74	aca gga aaa tat tac gcg atg gtg aca gga aaa gag ggt gaa ttt gaa				642
75	Thr Gly Lys Tyr Tyr Ala Met Val Thr Gly Lys Glu Gly Glu Phe Glu				
76	170	175	180		
78	caa tac gaa tta aag gcg gac aaa aat gga tac ata tcc ggc aaa aag				690
79	Gln Tyr Glu Leu Lys Ala Asp Lys Asn Gly Tyr Ile Ser Gly Lys Lys				
80	185	190	195	200	
82	gta cgg gcg ttt aaa atg aat tcc cag acg gaa ggg atg gca gca gac				738
83	Val Arg Ala Phe Lys Met Asn Ser Gln Thr Glu Gly Met Ala Ala Asp				
84	205	210	215		
86	gat gaa tac ggc agg ctt tat atc gca gaa gaa gat gag gcc att tgg				786
87	Asp Glu Tyr Gly Arg Leu Tyr Ile Ala Glu Glu Asp Glu Ala Ile Trp				
88	220	225	230		
90	aag ttc agc gcc gag ccg gac ggc agt aac gga acg gtt atc gac				834
91	Lys Phe Ser Ala Glu Pro Asp Gly Gly Ser Asn Gly Thr Val Ile Asp				
92	235	240	245		
94	cgt gcc gac ggc agg cat tta act cgt gat att gaa gga ttg acg att				882
95	Arg Ala Asp Gly Arg His Leu Thr Arg Asp Ile Glu Gly Leu Thr Ile				
96	250	255	260		
98	tac tac gct gct gac ggg aaa ggc tat ctg atg gca tca agc cag gga				930
99	Tyr Tyr Ala Ala Asp Gly Lys Gly Tyr Leu Met Ala Ser Ser Gln Gly				
100	265	270	275	280	
102	aac agc agc tac gcc att tat gac aga caa gga aag aac aaa tat gtt				978
103	Asn Ser Ser Tyr Ala Ile Tyr Asp Arg Gln Gly Lys Asn Lys Tyr Val				
104	285	290	295		
106	gcg gat ttt cgc ata aca gac ggt cct gaa aca gac ggg aca agc gat				1026
107	Ala Asp Phe Arg Ile Thr Asp Gly Pro Glu Thr Asp Gly Thr Ser Asp				
108	300	305	310		
110	aca gac gga att gac gtt ctg ggt ttc gga ctg ggg cct gaa tat ccg				1074
111	Thr Asp Gly Ile Asp Val Leu Gly Phe Gly Leu Gly Pro Glu Tyr Pro				
112	315	320	325		
114	tcc ggt att ttt gtc gca cag gac ggt gaa aat ata gat cac ggc caa				1122
115	Phe Gly Ile Phe Val Ala Gln Asp Gly Glu Asn Ile Asp His Gly Gln				
116	330	335	340		
118	aag gcc aat caa aat ttt aaa atc gtg cca tgg gaa aga att gct gat				1170
119	Lys Ala Asn Gln Asn Phe Lys Ile Val Pro Trp Glu Arg Ile Ala Asp				
120	345	350	355	360	
122	caa atc ggt ttc cgc ccg ctg gca aat gaa cag gtt gac ccg aga aaa				1218
123	Gln Ile Gly Phe Arg Pro Leu Ala Asn Glu Gln Val Asp Pro Arg Lys				

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124	365	370	375	
126	ctg acc gac aga agc gga aaa taaacatgca	aaaaggcagct	tataacaagct	1269
127	Leu Thr Asp Arg Ser Gly Lys			
128	380			
130	gctttttgca tgtgaagaac g			1290
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134	<211> LENGTH: 383			
135	<212> TYPE: PRT			
136	<213> ORGANISM: Bacillus subtilis; Strain: B13			
④=> 138	<400> SEQUENCE: 2			
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141	1 5 10 15			
144	Leu Thr Cys Gly Ala Val Ser Ser Gln Ala Lys His Lys Leu Ser Asp			
145	20 25 30			
148	Pro Tyr His Phe Thr Val Asn Ala Ala Ala Glu Thr Glu Pro Val Asp			
149	35 40 45			
152	Thr Ala Gly Asp Ala Ala Asp Asp Pro Ala Ile Trp Leu Asp Pro Lys			
153	50 55 60			
156	Thr Pro Gln Asn Ser Lys Leu Ile Thr Thr Asn Lys Lys Ser Gly Leu			
157	65 70 75 80			
160	Val Val Tyr Ser Leu Asp Gly Lys Met Leu His Ser Tyr Asn Thr Gly			
161	85 90 95			
164	Lys Leu Asn Asn Val Asp Ile Arg Tyr Asp Phe Pro Leu Asn Gly Lys			
165	100 105 110			
168	Lys Val Asp Ile Ala Ala Ser Asn Arg Ser Glu Gly Lys Asn Thr			
169	115 120 125			
172	Ile Glu Ile Tyr Ala Ile Asp Gly Lys Asn Gly Thr Leu Gln Ser Met			
173	130 135 140			
176	Thr Asp Pro Asp His Pro Ile Ala Thr Ala Ile Asn Glu Val Tyr Gly			
177	145 150 155 160			
180	Phe Thr Leu Tyr His Ser Gln Lys Thr Gly Lys Tyr Tyr Ala Met Val			
181	165 170 175			
184	Thr Gly Lys Glu Gly Glu Phe Glu Gln Tyr Glu Leu Lys Ala Asp Lys			
185	180 185 190			
188	Asn Gly Tyr Ile Ser Gly Lys Lys Val Arg Ala Phe Lys Met Asn Ser			
189	195 200 205			
192	Gln Thr Glu Gly Met Ala Ala Asp Asp Glu Tyr Gly Arg Leu Tyr Ile			
193	210 215 220			
196	Ala Glu Glu Asp Glu Ala Ile Trp Lys Phe Ser Ala Glu Pro Asp Gly			
197	225 230 235 240			
200	Gly Ser Asn Gly Thr Val Ile Asp Arg Ala Asp Gly Arg His Leu Thr			
201	245 250 255			
204	Arg Asp Ile Glu Gly Leu Thr Ile Tyr Tyr Ala Ala Asp Gly Lys Gly			
205	260 265 270			
208	Tyr Leu Met Ala Ser Ser Gln Gly Asn Ser Ser Tyr Ala Ile Tyr Asp			
209	275 280 285			
212	Arg Gln Gly Lys Asn Lys Tyr Val Ala Asp Phe Arg Ile Thr Asp Gly			
213	290 295 300			
216	Pro Glu Thr Asp Gly Thr Ser Asp Thr Asp Gly Ile Asp Val Leu Gly			

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Output Set: N:\CRF4\08302006\J669781A.raw

217	305	310	315	320													
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221					325				330						335		
224	Gly	Glu	Asn	Ile	Asp	His	Gly	Gln	Lys	Ala	Asn	Gln	Asn	Phe	Lys	Ile	
225					340				345					350			
228	Val	Pro	Trp	Glu	Arg	Ile	Ala	Asp	Gln	Ile	Gly	Phe	Arg	Pro	Leu	Ala	
229					355				360				365				
232	Asn	Glu	Gln	Val	Asp	Pro	Arg	Lys	Leu	Thr	Asp	Arg	Ser	Gly	Lys		
233					370				375				380				
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	244	1					5				10			15			
	247	Pro	Val	Asp	Thr	Ala	Gly	Asp	Ala	Ala							
	248				20				25								
E-->	251	<210>	SEQ ID NO:	<del>SEQ ID NO</del> 4													
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	259	1					5				10			15			
	262	Pro	Val	Asp	Thr	Ala	Gly	Asp	Ala	Ala	Asp	Asp	Pro	Ala	Ile	Leu	Asp
	263				20				25				30				
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	274	1				5											
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	284	Glu	Gly	Glu	Phe	Glu	Gln	Tyr	Glu	Leu	Lys						
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	296	1				5											
E-->	299	<210>	SEQ ID NO:	<del>SEQ ID NO</del> 8													

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/10/669,781A

DATE: 08/30/2006  
TIME: 10:14:34

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Output Set: N:\CRF4\08302006\J669781A.raw

300 <211> LENGTH: 6  
301 <212> TYPE: PRT  
302 <213> ORGANISM: Bacillus subtilis  
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307 1 5  
E--> 310 <210> SEQ ID NO: ~~SEQ\_ID\_NO:9~~  
311 <211> LENGTH: 25  
312 <212> TYPE: PRT  
313 <213> ORGANISM: Bacillus subtilis  
E-> 315 <400> SEQUENCE: 9  
317 Ile Val Pro Trp Glu Arg Ile Ala Asp Gln Ile Gly Phe Arg Pro Leu  
318 1 5 10 15  
321 Ala Asn Glu Gln Val Asp Pro Arg Lys  
322 20 25  
E--> 325 <210> SEQ ID NO: ~~SEQ\_ID\_NO:10~~  
326 <211> LENGTH: 30  
327 <212> TYPE: PRT  
328 <213> ORGANISM: Bacillus subtilis  
E-> 330 <400> SEQUENCE: 10  
332 Asn Gly Thr Leu Gln Ser Met Thr Asp Pro Asp His Pro Ile Ala Thr  
333 1 5 10 15  
336 Ala Ile Asn Glu Val Tyr Gly Phe Thr Leu Trp His Ser Gln  
337 20 25 30  
E--> 340 <210> SEQ ID NO: ~~SEQ\_ID\_NO:11~~  
341 <211> LENGTH: 23  
342 <212> TYPE: PRT  
343 <213> ORGANISM: Bacillus subtilis  
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347 Tyr Val Ala Asp Phe Arg Ile Thr Asp Gly Pro Glu Thr Asp Gly Thr  
348 1 5 10 15  
351 Ser Asp Asp Asp Gly Ile Ile  
352 20  
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356 <211> LENGTH: 7  
357 <212> TYPE: PRT  
358 <213> ORGANISM: Bacillus subtilis  
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362 Leu Thr Asp Arg Ser Gly Lys  
363 1 5  
E--> 366 <210> SEQ ID NO: ~~SEQ\_ID\_NO:13~~  
367 <211> LENGTH: 13  
368 <212> TYPE: PRT  
369 <213> ORGANISM: Bacillus subtilis  
E-> 371 <400> SEQUENCE: 13  
373 Val Asp Ile Ala Ala Ala Ser Asn Arg Ser Glu Gly Lys  
374 1 5 10  
E--> 377 <210> SEQ ID NO: ~~SEQ\_ID\_NO:14~~  
378 <211> LENGTH: 19

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/669,781A

DATE: 08/30/2006

TIME: 10:14:34

Input Set : F:\6031.79428 sequence.listing.ST25.txt  
Output Set: N:\CRF4\08302006\J669781A.raw

379 <212> TYPE: PRT  
380 <213> ORGANISM: Bacillus subtilis  
E--> 382 <400> SEQUENCE: 14  
384 Ile Ala Asp Gln Ile Gly Phe Arg Pro Leu Ala Asn Glu Gln Val Asp  
385 1 5 10 15  
388 Pro Arg Lys  
E--> 392 <210> SEQ ID NO: SEQ\_ID\_NO+15  
393 <211> LENGTH: 6  
394 <212> TYPE: PRT  
395 <213> ORGANISM: Bacillus subtilis  
E--> 397 <400> SEQUENCE: 15  
399 Ala Asn Gln Asn Phe Lys  
400 1 5  
E--> 403 <210> SEQ ID NO: SEQ\_ID\_NO+16  
404 <211> LENGTH: 5  
405 <212> TYPE: PRT  
406 <213> ORGANISM: Bacillus subtilis  
E--> 408 <400> SEQUENCE: 16  
410 Val Arg Ala Phe Lys  
411 1 5  
E--> 414 <210> SEQ ID NO: SEQ\_ID\_NO+17  
415 <211> LENGTH: 11  
416 <212> TYPE: PRT  
417 <213> ORGANISM: Bacillus subtilis  
E--> 419 <400> SEQUENCE: 17  
421 Leu Asn Asn Val Asp Ile Arg Tyr Asp Phe Pro  
422 1 5 10  
E--> 425 <210> SEQ ID NO: SEQ\_ID\_NO+18  
426 <211> LENGTH: 15  
427 <212> TYPE: PRT  
428 <213> ORGANISM: Bacillus subtilis  
E--> 430 <400> SEQUENCE: 18  
432 Leu Asn Asn Val Asp Ile Arg Tyr Asp Phe Pro Leu Asn Gly Lys  
433 1 5 10 15  
E--> 436 <210> SEQ ID NO: SEQ\_ID\_NO+19  
437 <211> LENGTH: 11  
438 <212> TYPE: PRT  
439 <213> ORGANISM: Bacillus subtilis  
E--> 441 <400> SEQUENCE: 19  
443 Asn Thr Ile Glu Ile Tyr Ala Ile Asp Gly Lys  
444 1 5 10  
E--> 447 <210> SEQ ID NO: SEQ\_ID\_NO+20  
448 <211> LENGTH: 11  
449 <212> TYPE: PRT  
450 <213> ORGANISM: Bacillus subtilis  
E--> 452 <400> SEQUENCE: 20  
454 Ser Gly Leu Val Val Tyr Ser Leu Asp Gly Lys  
455 1 5 10  
E--> 458 <210> SEQ ID NO: SEQ\_ID\_NO+21

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/10/669,781A

DATE: 08/30/2006  
TIME: 10:14:34

Input Set : F:\6031.79428 sequence.listing.ST25.txt  
Output Set: N:\CRF4\08302006\J669781A.raw

```

459 <211> LENGTH: 22
460 <212> TYPE: PRT
461 <213> ORGANISM: Bacillus subtilis
@-> 463 <400> SEQUENCE: 21
465 Phe Ser Ala Glu Pro Asp Gly Gly Ser Asn Gly Thr Val Ile Asp Arg
466 1           5           10          15
469 Ala Asp Gly Arg His Leu
470      20
E--> 473 <210> SEQ ID NO: SEQ_ID_NO:22
474 <211> LENGTH: 23
475 <212> TYPE: DNA
476 <213> ORGANISM: Artificial
478 <220> FEATURE:
479 <223> OTHER INFORMATION: Synthesized
482 <220> FEATURE:
483 <221> NAME/KEY: modified_base
484 <222> LOCATION: (1)..(23)
485 <223> OTHER INFORMATION: All Ns represents inosine
@X-> 487 <400> SEQUENCE: 22
W--> 488 tcngatccnt atcattttac ngt                                23
E--> 491 <210> SEQ ID NO: SEQ_ID_NO:23
492 <211> LENGTH: 23
493 <212> TYPE: DNA
494 <213> ORGANISM: Artificial
496 <220> FEATURE:
497 <223> OTHER INFORMATION: Synthesized
500 <220> FEATURE:
501 <221> NAME/KEY: modified_base
502 <222> LOCATION: (1)..(23)
503 <223> OTHER INFORMATION: N represents inosine
@K-> 506 <400> SEQUENCE: 23
507 agmggaaaaat catancyrat atc                                23
E--> 510 <210> SEQ ID NO: SEQ_ID_NO:24
511 <211> LENGTH: 22
512 <212> TYPE: DNA
513 <213> ORGANISM: Artificial
515 <220> FEATURE:
516 <223> OTHER INFORMATION: Synthesized
518 <220> FEATURE:
519 <221> NAME/KEY: modified_base
520 <222> LOCATION: (1)..(22)
521 <223> OTHER INFORMATION: All N's represent inosine
@L-> 523 <400> SEQUENCE: 24
524 cttcnganck rttnangcn gc                                22
E--> 527 <210> SEQ ID NO: SEQ_ID_NO:25
528 <211> LENGTH: 20
529 <212> TYPE: DNA
530 <213> ORGANISM: Artificial
532 <220> FEATURE:

```

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/10/669,781A

DATE: 08/30/2006  
TIME: 10:14:34

Input Set : F:\6031.79428 sequence.listing.ST25.txt  
Output Set: N:\CRF4\08302006\J669781A.raw

533 <223> OTHER INFORMATION: Synthesized  
 536 <220> FEATURE:  
 537 <221> NAME/KEY: modified\_base  
 538 <222> LOCATION: (1)..(20)  
 539 <223> OTHER INFORMATION: All N's represent inosine  
 541 <400> SEQUENCE: 25  
 542 tgatcngcra tnckttccca  
 E--> 545 <210> SEQ ID NO: ~~SEQ-ID NO+26~~ 20  
 546 <211> LENGTH: 20  
 547 <212> TYPE: DNA  
 548 <213> ORGANISM: Artificial  
 550 <220> FEATURE:  
 551 <223> OTHER INFORMATION: Synthesized  
 553 <400> SEQUENCE: 26  
 554 gcratmggat gatcmggatc  
 E--> 557 <210> SEQ ID NO: ~~SEQ-ID NO+27~~ 20  
 558 <211> LENGTH: 21  
 559 <212> TYPE: DNA  
 560 <213> ORGANISM: Artificial  
 562 <220> FEATURE:  
 563 <223> OTHER INFORMATION: Synthesized  
 566 <220> FEATURE:  
 567 <221> NAME/KEY: modified\_base  
 568 <222> LOCATION: (1)..(21)  
 569 <223> OTHER INFORMATION: N represents inosine  
 571 <400> SEQUENCE: 27  
 572 ttcataytgt tcaaattcnc c 21  
 E--> 575 <210> SEQ ID NO: ~~SEQ-ID NO+28~~  
 576 <211> LENGTH: 26  
 577 <212> TYPE: DNA  
 578 <213> ORGANISM: Artificial  
 580 <220> FEATURE:  
 581 <223> OTHER INFORMATION: Synthesized  
 584 <220> FEATURE:  
 585 <221> NAME/KEY: modified\_base  
 586 <222> LOCATION: (1)..(26)  
 587 <223> OTHER INFORMATION: All N's represent inosine  
 589 <400> SEQUENCE: 28  
 590 ttnccngtrt tatangaatg narcat 26  
 E--> 593 <210> SEQ ID NO: ~~SEQ-ID NO+29~~  
 594 <211> LENGTH: 20  
 595 <212> TYPE: DNA  
 596 <213> ORGANISM: Artificial  
 598 <220> FEATURE:  
 599 <223> OTHER INFORMATION: Synthesized  
 602 <220> FEATURE:  
 603 <221> NAME/KEY: modified\_base  
 604 <222> LOCATION: (1)..(20)  
 605 <223> OTHER INFORMATION: N represents inosine

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/10/669,781A

DATE: 08/30/2006  
TIME: 10:14:34

Input Set : F:\6031.79428 sequence.listing.ST25.txt  
Output Set: N:\CRF4\08302006\J669781A.raw

```

@> 607 <400> SEQUENCE: 29
608 ccatcratng catarattc
E--> 611 <210> SEQ ID NO: SEQ ID NO:30 20
612 <211> LENGTH: 18
613 <212> TYPE: DNA
614 <213> ORGANISM: Artificial
616 <220> FEATURE:
617 <223> OTHER INFORMATION: Synthesized
620 <220> FEATURE:
621 <221> NAME/KEY: modified_base
622 <222> LOCATION: (1)..(18)
623 <223> OTHER INFORMATION: N represents inosine
@> 626 <400> SEQUENCE: 30
627 tttaaarttgygrttngc
E--> 630 <210> SEQ ID NO: SEQ ID NO:31 18
631 <211> LENGTH: 18
632 <212> TYPE: DNA
633 <213> ORGANISM: Artificial
635 <220> FEATURE:
636 <223> OTHER INFORMATION: Synthesized
639 <220> FEATURE:
640 <221> NAME/KEY: modified_base
641 <222> LOCATION: (1)..(18)
642 <223> OTHER INFORMATION: All N's represent inosine
@> 645 <400> SEQUENCE: 31
646 tttncnngtn accatngc
E--> 649 <210> SEQ ID NO: SEQ ID NO:32 18
650 <211> LENGTH: 38
651 <212> TYPE: DNA
652 <213> ORGANISM: Artificial
654 <220> FEATURE:
655 <223> OTHER INFORMATION: Synthesized
658 <220> FEATURE:
659 <221> NAME/KEY: misc_feature
660 <222> LOCATION: (21)..(21)
661 <223> OTHER INFORMATION: n is a, c, g, or t
@> 663 <400> SEQUENCE: 32
664 gayccdtayc aytyyacdgtaaaygcgacd gcdgaaaac
E--> 667 <210> SEQ ID NO: SEQ ID NO:33 38
668 <211> LENGTH: 52
669 <212> TYPE: DNA
670 <213> ORGANISM: Artificial
672 <220> FEATURE:
673 <223> OTHER INFORMATION: Synthesized
676 <220> FEATURE:
677 <221> NAME/KEY: misc_feature
678 <222> LOCATION: (7)..(14)
679 <223> OTHER INFORMATION: Mfe I site
681 <220> FEATURE:

```

RAW SEQUENCE LISTING DATE: 08/30/2006  
PATENT APPLICATION: US/10/669,781A TIME: 10:14:34

**Input Set : P:\6031.79428 sequence.listing.ST25.txt**  
**Output Set: N:\CRF4\08302006\J669781A.raw**

682 <221> NAME/KEY: RBS  
683 <222> LOCATION: (14)..(19)  
685 <220> FEATURE:  
686 <221> NAME/KEY: CDS  
687 <222> LOCATION: (27)..(50)  
689 <400> SEQUENCE: 33  
690 gtttctcaat tgaaggagga atttaa atg ctg tcc gat cct tat cat ttt ac  
691 Met Leu Ser Asp Pro Tyr His Phe  
692 1 5  
E--> 695 <210> SEQ ID NO: ~~SEQ\_ID\_NO+34~~  
696 <211> LENGTH: 8  
697 <212> TYPE: PRT  
698 <213> ORGANISM: Artificial  
700 <220> FEATURE:  
701 <223> OTHER INFORMATION: Synthetic Construct  
OK-> 703 <400> SEQUENCE: 34  
705 Met Leu Ser Asp Pro Tyr His Phe  
706 1 5  
E--> 709 <210> SEQ ID NO: ~~SEQ\_ID\_NO+35~~  
710 <211> LENGTH: 35  
711 <212> TYPE: DNA  
712 <213> ORGANISM: Artificial  
714 <220> FEATURE:  
715 <223> OTHER INFORMATION: Synthesized  
718 <220> FEATURE:  
719 <221> NAME/KEY: misc\_feature  
720 <222> LOCATION: (6)..(11)  
721 <223> OTHER INFORMATION: Sal I site  
OK-> 723 <400> SEQUENCE: 35  
724 aataagtctcgatcgacccg gattccggct gtgcgt  
E--> 727 <210> SEQ ID NO: ~~SEQ\_ID\_NO+36~~  
728 <211> LENGTH: 34  
729 <212> TYPE: DNA  
730 <213> ORGANISM: Artificial  
732 <220> FEATURE:  
733 <223> OTHER INFORMATION: Synthesized  
736 <220> FEATURE:  
737 <221> NAME/KEY: misc\_feature  
738 <222> LOCATION: (6)..(11)  
739 <223> OTHER INFORMATION: Bgl II site  
OK-> 741 <400> SEQUENCE: 36  
742 aataaaqatc ttttccgct tctgtccggtc agtt

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VERIFICATION SUMMARY DATE: 08/30/2006  
PATENT APPLICATION: US/10/669,781A TIME: 10:14:35

Input Set : F:\6031.79428 sequence.listing.ST25.txt  
Output Set: N:\CRF4\08302006\J669781A.raw

L:17 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO  
L:27 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:1  
L:133 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO  
L:138 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:2  
L:236 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO  
L:241 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:3  
L:251 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO  
L:256 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:4  
L:266 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO  
L:271 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:5  
L:277 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO  
L:282 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:6  
L:288 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO  
L:293 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:7  
L:299 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO  
L:304 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:8  
L:310 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO  
L:315 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:9  
L:325 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO  
L:330 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:10  
L:340 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO  
L:345 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:11  
L:355 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO  
L:360 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:12  
L:366 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO  
L:371 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:13  
L:377 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO  
L:382 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:14  
L:392 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO  
L:397 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:15  
L:403 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO  
L:408 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:16  
L:414 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO  
L:419 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:17  
L:425 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO  
L:430 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:18  
L:436 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO  
L:441 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:19  
L:447 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO  
L:452 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:20  
L:458 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO  
L:463 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:21  
L:473 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO  
L:487 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:22  
L:488 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22 after pos.:0  
L:491 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO  
L:506 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:23  
M:341 Repeated in SeqNo=0

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VERIFICATION SUMMARY

PATENT APPLICATION: US/10/669,781A

DATE: 08/30/2006

TIME: 10:14:35

Input Set : F:\6031.79428 sequence.listing.ST25.txt  
Output Set: N:\CRF4\08302006\J669781A.raw

L:510 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO  
L:523 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:24  
L:527 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO  
L:541 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:25